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A;Experimental source: strain 972h-; cosmid c9E9
                                                                                                                                                                                                                                                                                                                                           9
                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                                                                                               Length 758;
                                                                                                                                                                                                                                                                                                              61.0%; Score 2473.5; DB 2; Length 62.9%; Pred. No. 4.7e-165; ive 92; Mismatches 172; Indels
                                                                                                                        Wood,
                                                                                                                                                                                                                                                        A;Gene: leu2; SPDB:SPAC9E9.03
A;Map position: 1
C;Superfamily: iron-responsive element-binding protein
                                                                                                    C. Accession: T39210
R:McDougall, R.; Barrell, B.G.; Rajandream, M.A.; We wendirted to the EMBL Data Library, September 1997
A;Reference number: 221836
A;Accession: T39210
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-758 <MCD>
ALIGNMENTS
                                                                 fission yeast
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.9°
Matches 489; Conservative
                                                                  3-isopropylmalate dehydratase
                                                                                                                                                                                                                                              Genetics:
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A;Accession: S6401

A;Molecule type: DNA

A;Residues: 1-779 cHBB>

A;Cross-references: EMBL:Z72531; NID:g1322462; PIDN:CAA96709.1; PID:g1322463; MIPS:YC

A;Experimental source: strain S288C

A;Experimental source: strain S288C

K;Skala, J.; Capieaux, E.; Balzi, E.; Chen, W.; Goffeau, A.

Yeast 7, 281-285, 1991

A;Title: Complete sequence of the Saccharomyces cerevisiae LEU1 gene encoding isoprop

A;Reference number: S15039; MUID:91353082; PMID:1840714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-48 <HSUS
A; Residues: 1-48 <HSUS
A; Residues: EMBL:K01969; NID:g171834; PIDN:AAA34742.1; PID:g171835
A; Crosos-references: EMBL:K01969; NID:g171834; PIDN:AAA34742.1; PID:g171835
B; Chan, W.; Balzi, E.; Capieaux, E.; Choder, M.; Goffeau, A.
Yeast 7, 287-299, 1991
A; Title: The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1
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                                                                                                                                                                                                                                                                                                                                   3-isopropylmalate dehydratase (EC 4.2.1.33) - yeast (Saccharomyces cerevisiae) N;Alternate names: isopropylmalate isomerase; protein G3734; protein YGL009c C;Species: Saccharomyces cerevisiae C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000 C;Accession: S64011; S15039; A24105; S31555 R;Hebling, U; Hofmann, B.; Delius, H. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hsu, Y.P.; Schimmel, P.
J. Biol. Chem. 259, 3714-3719, 1984
A;Title: Yeast LEUI. Repression of mRNA levels by leucine and relationship of A;Reference number: A24105; MUID:84162042; PMID:6323436
A;Accession: A24105
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653 LPIPTPIE-QVNDMMKAAENQVKFSVDLVNQTI--TYGDKQVKFDVEPFRKHCLVNGLDD 709
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A;Experimental Bource: strain IL125-28
B;HSU, Y.P.; Schimmel, P.
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                                                                          IGLTMOMEDKIAEFEAKMTRETPWLDGTGYLKRKGQGGKLAAKAVPVPTTNRGEEKKE 774
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A;Reference number: $15040; MUID:91353083; PMID:1882553
A;Accession: $31555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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;Superfamily: iron-responsive element-binding protein
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larity 63.1%; Pred. No. 7.6e-164;
Conservative 93; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SGD:LEU1
A;Cross-references: SGD:S0002977; MIPS:YGL009c
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A;Residues: 740-743,'K',745-779 <CHE>
A;Cross-references: GB:SS8126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S64003
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RESULT 3
236864
3-isopropylmalate dehydratase (EC 4.2.1.33) - Phycomyces blakesleeanus
3-isopropylmalate dehydratase (EC 4.2.1.33) - Phycomyces blakesleeanus
N,Alternate names: alpha-IPM isomerase; alpha-isopropylmalate isomerase
C;Species: Phycomyces blakesleeanus
C;Accies: Phycomyces blakesleeanus
C;Accession: S26864; S10998
R;Iturriaga, E.A.; Dlaz-Minguez, J.M.; Benito, E.P.; Alvarez, M.I.; Eslava,
R;Iturriaga, E.A.; Dlaz-Minguez
A;Title: Heterologous transformation of Mucor circinelloides with the Phycor
A;Reference number: S26864; MUID:92224296; PMID:1563047
A;Accession: S26864
A;Status: not compared with conceptual translation
A;Molecule type: DMA
A, Page 1488 A TMIN
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-689 <IT2>
A;Cross-references: EMBL
C;Genetics:
A;Gene: leul
C;Superfamily: homoaconi
C;Keywords: carbon-oxyge
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                                                                                                                                              A;Residues: 1-689 < ITU>
R;Iturriaga, E.A.; Diaz-Minguez, C.
Nuccleic Acids Res. 18, 4612, 1990
A;Title: Nucleotide sequence of th
A;Reference number: S10998; MUID: A;Accession: S10998
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     Superfamily: homoaconitate hydratase; Keywords: carbon-oxygen lyase; hydro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKLTDYK----
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   carbon-oxygen
                                                                            EMBL: X53090;
                                                                                                                                                                 of the Phycomyces blakesleeanus
MUID:90356419; PMID:2388845
                                                                                                                                                                                                                   J.M.; Benito,
     hydro-lyase;
                                                                          NID: 93112;
                                                                             PIDN: CAA37257
       leucine
                                                                                                                                                                                                                     E.P.; Alvarez,
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       biosynthesis
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A; Molecule type: DNA
A; Residues: 1-644 <RON>
A; Residues: 1-644 <RON>
A; Cross-references: GB:M33166; NID:g168366; PIDN:AAA33422.1;
A; Cross-references: GB:M33166; NID:g168366; PIDN:AAA33422.1;
A; Note: the authors translated the codon ATT for residue 119
A; Note: the authors translated the codon ATT for residue 119
Curr. Genet. 21, 215-223, 1992
A; Title: Heterologous transformation of Mucor circinelloides
A; Reference number: S26864; MUID:92224296; PMID:1563047
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                                                                                                                                      Gene 84, 335-343, 1989
A; Title: Characterization of A; Reference number: JQ0160; A; Accession: JQ0160
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                                                                                                                                                                                                                                                           3-isopropylmalate dehydratase (EC 4.2.1.33) - Rhizomucor circinelloides
N;Alternate names: alpha-isopropylmalate isomerase
C;Species: Rhizomucor circinelloides
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Best Local S
Matches 472
                                                                                                                                                                                                       ;Date: 07-Sep-1990 #sequence_revision;Accession: JQ0160; S26865;Roncero, M.I.G.; Jepsen, L.P.; Strome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPPPKFQTI-QPKVEDEAAHKQAADQADPVTDCPP--AGSPVNKGAPV--ASAMPAFTTL
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                                                                                                                                                            of a leuA gene and an ARS element 0; MUID:90128278; PMID:2693214
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No. 1.4e-157;
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A;Accession: C97684
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-475 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88428.1; PID:g15157923; GSPDB:GN00169
C;Genetics:
                                                                                                                                                                                                                                                                                                                      66 TIDHNVPITSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGP 125
                                                                                                                                                                                                                                                                                                  EQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
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                                                                                                                                                                                62 VVDHNVPTS-----PDRINGIQNEESRIQVEALARNAADFGVEYYSERDKRQGIVHIVGP
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39.1%; Score 1586; DB 2; Sest Local Similarity 65.3%; Pred. No. 3.4e-103; Matches 311; Conservative 52; Mismatches 105;
                                                                                      39.7%; Score 1611; DB 2; 66.8%; Pred. No. 5.9e-105;
                                                                                                                         51; Mismatches
A;Gene: BME10157
A;Map position: In.
S:Superfamily: aconitate hydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase
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A;Map position: circular chromosome
C;Superfamily: aconitate hydratase
                                                                                                      Best Local Similarity 66.89
Matches 316; Conservative
                                                                                        Query Match
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C'Accession: AH327,

Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Accession: AH327

A;Eference number: AD3222; PMID:11756688

A;Residues: preliminary

A;Residues: 1-469 <kUR>
A;Residues: 1-469 <kUR>
A;Esperimental source: strain 16M

C;Senetics:
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                                                                   of leucine
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         A Status: not compared with conceptual translation A; Molecule type: DNA A; Residues: 1-644 <ITU>
C; Comment: This enzyme is involved in the biosynthesis of Genetics: A; Genetics: C; Homoaconitate hydratase C; Keywords: carbon-oxygen lyase; hydro-lyase
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A;Residues: 1-469 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43690.1; PID:g17741217; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: AD2909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: The Genome of the Natural Genetic Engineer A; Reference number: AB2577; PMID:11743193
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

Science 294, 2317-2323, 2001
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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Best Local Similarity
Matches 310; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCLAMNDDRLKPGERCASTSNRNFEGRQGYKSRTHLVSPAMAAAAAIAGHFVDVRE 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCLGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRIEDLRAAAKIVDGRKVASTV-SAMIVPGSGLVKEQAEKEGLDKIFLDAGFEWREPGCS
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APDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWG
                                                                                                                                                                                                                                                                                                                                    STPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLA 65
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                                                                                       LAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMV 245
                                                                                                                                                                            EQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
                                                                                                                                                                                                                        VVDHNVPTTA-----DRLEGIKNEESRIQVEALAQNAKEFGVEYYSERDKRQGIVHIVGP 116
                                                                                                                                                                                                                                                                 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGP 125
                                                                                                                                                                                                                                                                                                             SAPRTLYDKIWDDHVVNRDPDGTCLLYIDRHLVHEVTSPQAFEGLRIAGRPVHSPTRTLA
                                           LPESVTAKDIILAIIGEIGTAGGTGHVIEFAGEAIRSLSMEGRMTVCNWTIEGGARAGLI 236
                                                                                                                                   EQGFTLPGMTIVCGDSHTSTHGAFGALAHGIGTSEVEHVLATQTLIQKKAKNMLVRVDGK 176
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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3-isopropylmalate dehydratase, large subunit [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: C87273 R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolong, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Superfamily: aconitate hydratase
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A; Residues: 1-479 < STO>
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                            MCLGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL
                                                                                                                                                                                                                                                                     DKTFAYIQGKPAAPK--GAAWDMALSHWKTFFTDEDAVFDRTVVIDGSALVPMVTWGTSP
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MCLAMNPDKLAPQERCASTSNRNFEGRQGRAGRTHLVSPAMAAAAAIAGHLVDVRTL
                                                                                                                                                                                                          EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIFVDKVFIGSCTNSRIED
                                                                                                                                                                                                                                                                                                               EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP
                                                                                                                                                                                                                                                                                                                                                                 GVTGKDVALAVIGEIGTAGGTGYVIEFAGEAIAGLSMEGRMTLCNLTIEGGAKAGLVAPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
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                                                                                           MRAAAAVVQEAFLHGRLVAPHVK-AMVVPGSGLVKEQAEEEGLDAIFKAAGFDWREPGCS
                                                                                                                                   LRAAAAVVK-----GRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCS 423
                                                                                                                                                                                EDVIPVIGNVPDPESFÄTPDKRAAAHRALDYMGLKAGQPISEARIDRVFIGSCTNSRIED
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Similarity 64.4%;
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Pred. No. 1.6e-101;
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A/Molecule type: DNA
A/Residues: 1-469 <PAR>
A/Residues: 1-469 <PAR>
A/Cross-references: GB.AL162756; GB.AL157959; NID:g7380091; PIDN:CAB84686.1; PID:g738
A/Experimental source: serogroup A, strain Z2491
C/Genetics: A/Gene: leuC; NWA1450
C/Superfamily: aconitate hydratase
C/Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFG-VTYFGLSDKRQGIVHVIGP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGE 185
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                                                                                                                                                                                                                                                                             Query Match
38.1%; Score 1545.5; DB 2; Length
Best Local Similarity 63.4%; Pred. No. 2.3e-100;
Matches 301; Conservative 62; Mismatches 103; Indels
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A,Molecule type: DNA
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Matches 295;
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Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
Rifetceln. H; Saunders, N.J; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Aterian gall28
A;Accession: Gall28
A;Accession: Gall28
A;Accession: Gall28
A;Residues: 1-469 <a href="https://documents.org/lines/lines/">ArET>
A;Residues: I-469 <a href="https://documents.org/">ArET>
A;Residues: I-469 <a href="https://documents.org/">ArET>
A;Residues: I-469 <a href="https://documents.org/">ArET>
A;Residues: Gall28
A;Cross-references: Ga
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S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
                                                           3-isopropylmalate dehydratase, large chain NMB1036 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morr; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrear Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [imported]
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 38.2%; Score 1548.5; DB 2; Length Best Local Similarity 63.6%; Pred. No. 1.4e-100; Matches 302; Conservative 62; Mismatches 102; Indels
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Gene: NMB1036
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3-isopropylmalate dehydratase large subunit PA3121 [imported] - Pseudomonas aeruginos C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Dsep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G8255 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J., adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE004091; NID:g9949227; PIDN:AAG06509.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%; Score 1507.5; DB 2; ilarity 62.5%; Pred. No. 1.1e-97; Conservative 61; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1474 <2TO>
A;Cross-references: GB:AE004736; GE
A;Experimental source: strain PAO1
A;Genetics: PA3121
C;Superfamily: aconitate hydratase
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A,Experimental source: strain 9a5c

A,Experimental source: strain 9a5c

R,Simpson, A,J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H Briones, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-orry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins, E.A.; Machinors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.S.; Silva, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.J., da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.J., da Silva, A.J.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel A;Accession: H82564
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R;anonymous, The Xyle
Nature 406, 151-157,
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A;Molecule type: DNA
A;Residues: 1-474 <SIM>
A;Cross-references: GB:AE004047; GB:AE003849; NID:g9107548; PIDN:AAF85174.1; GSPDB:GN00
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C;Date: 18-Aug-2000 #sequence_revision
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A,Cross-references: GB:AE000117; GB:U00096; NID:g1786250; A;Experimental source: strain K-12, substrain MG1655 R;Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; submitted to the EMBL Data Library, December 1992 A;Description: Systematic sequencing of the Escherichia co
                                                                                                                                                                                                                                                                                                              Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64728
                                                                                                                                                                                                                                                                                                                                                                                G;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-
C;Accession: H64728; S40586; S41198; S43708
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
.A.; Rose, D.J.; Mau, B.; Shao, Y.
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   the
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K-12)

A;Molecule type: DNA
A;Residues: 1-70, 'G', 72-361, 'V', 363-466 <YUR>
A;Residues: 1-70, 'G', 72-361, 'V', 363-466 <YUR>
A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA0134
A;Experimental source: Escherichia coli K-12
R;Kirino, H.; Aoki, M.; Aoshima, M.; Hayashi, Y.; Ohba, M.
Eur. J. Biochem. 220, 275-281, 1994
A;Title: Hydrophobic interaction at the subunit interface
A;Reference number: S41197; MUID:94164169; PMID:8119295
A;Accession: S41198 A;Experimental source: strain K-12 R;Kirino, H.; Aoki, M.; Hayashi, Y.; submitted to the EMBL Data Library, A; Molecule type: A; Residues: 1-73, A; Accession: A; Reference number: S43708 A;Residues: 1-204 <KIR1> A;Cross-references: EMBL:D17631 A; Molecule type: DNA S43708 , 'G' ,75-204 ; Ohba, M.; September **⊠** Yamagishi, PIDN:AAC73183.1; PID:g1786259; Yamagishi, A.; Wakagi, T.; Wakagi, of f K.; Mizobuc

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Fightis:

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                                                                                                                                                                                                                                                                                 117 VTLPGMT1VCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKTMKIEVTGNAAP
                                                              FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP
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                                                                                                                                           HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG
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Pred. No. 3.8e-95;
2; Mismatches 112;
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Best Local Similarity 59.4%; Pre
Matches 281; Conservative 72;
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L.; White, N.; Farrar,
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A,Cross-references: EMBL:D17631; NID:g409068; PID:g2160235
A,Experimental source: strain K-12 .
Genetics:
A,Genetics:
A,Gene: leuC
C,Function:
A,Pathway: leucine biosynthesis
A,Suberfamily: aconitate hydratase
C,Keywords: 4Fe-4S, carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine P;347,407,410/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: AD0516
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella & A; Reference number: AB0502; PMID:11677608
A; Recession: AD0516
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-466 < PAR>
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                           68
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                                                                                                                                                                                                                                                                              DB 2; Length
                                                                                                                                                                                                                                                                           36.5%; Score 1479.5; DB 2; Length 62.1%; Pred. No. 9.5e-96; ive 59; Mismatches 111; Indels
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Best Local Similarity 62.1<sup>§</sup>
Matches 293; Conservative
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Matches 291; Conservative
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: D90638
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90638
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A; Molecule type: DNA
A; Residues: 1-466 <HAY>
A; Cross-references: GB: BA000007; PIDN: BAB33499.1; PID:
A; Cross-references: strain O157:H7, substrain RIMD
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                                                               ETTENYVKGRLHAPK--GKDFDDAVAYWKTLQTDEGATFDTVVTLQAEEISPQVTWGTNP
                                                                                             EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
                                                                                                                                   ĠITAKDIVLAIIGKTGSAGGTGHVVEFCGEAIRDLSMEGRMTLCNMAIEMGAKAGLVAPD
                                                                                                                                                                GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD
                                                                                                                                                                                                      VTLPGMTIVCGDSHTATHGAFGALAFGIGTSEVEHVLATQTLKQGRAKTMKIEVQGKAAP
                                                                                                                                                                                                                                       FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
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Pred. No. 4.7e-95;
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RESULT 18
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C;Accession: AI0065
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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A; Residues: 1-466 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, lerna, N.T.; Contago, J.D.; Rose, lerna, N.J.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Residues: 1-476 <KUR>
A;Residues: 1-476 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89388.1; PID:g15978624; GSPDB:GN00175
C;Genetics:
A;Genetics:
C;Superfamily: aconitate hydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-isopropylmalate dehydratase, large chain VC2492 [similarity] - Vibrio cholerae (strai. C. Species Vabrio cholerae (c. Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: H82070 #sequence_revision W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. Rathe: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833; PMID:10952301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKTFAIMDHNVSTQT----KDINA--SGEMARIQMQELIKUKAEFGVSLYDLNHPFQGIV
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                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                        Query Match
35.8%; Score 1452; DB 2; Length 4'
Best Local Similarity 59.2%; Pred. No. 8.2e-94;
Matches 289; Conservative 66; Mismatches 121; Indels
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A;Molecule type: DNA
A;Residues: 1-467 <HEI>
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3-isopropylmalate dehydratase (EC 4.2.1.33) large chain - Actinoplanes teichomycetic 3-isopropylmalate isomerase large chain NiAlternate names: isopropylmalate isomerase large chain C; Species: Actinoplanes teichomyceticus C; Species: Actinoplanes teichomyceticus C; Species: Joul-1996 #sequence_revision 19-Jul-1996 #text_change 24-Nov-1999 C; Accession: 136699 #sequence_revision 19-Jul-1996 #text_change 24-Nov-1999 C; Accession: 13699; Mulp: Species: Borghi, A.; Sosio, M. Gene 158, 77-100, 1995 A; Mulp: Species: Indianation of a Streptomyces lividans Leu- mutant by the Actinoplanes A; Reference number: 139699; Mulp: 95309734; PMID: 7789819 A; Residues: 139699; Mulp: 95309734; PMID: 7789819 A; Molecule type: DNA A; Mo
PIDN:AAF95634.1; GSPDB:G
El Tor
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(covalent) #status predicted
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34.8%; Score 1413; DB 2; Length 4
Best Local Similarity 59.7%; Pred. No. 4.6e-91;
Matches 285; Conservative 51; Mismatches 125; Indels
                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                               Indels
      GB:AE003852; NID:g9657063;
O1; strain N16961; biotype
                                                                                                                                                                                                                               ; Score 1425.5; DB 2;
; Pred. No. 5.7e-92;
67; Mismatches 119;
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C;Superfamily: aconitete hydratase
C;Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase;
F;367,427,430/Binding site: 4Fe-4S cluster (Cys) (cova
          A, Cross-references: GB:AE004318; GI
A, Experimental source: serogroup O:
C, Genetics:
A, Gene: VC2492
A, Map position: 1
C, Superfamily: aconitate hydratase
                                                                                                                                                                                                                                      35.2%;
llarity 58.9%;
Conservative 67
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Best Local Simi
Matches 279;
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A;Cross-references: GB:AP001517; GB:BA0000004; NID:g10175500; PIDN:BAB06775.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nuccleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision
C;Accession: H84031
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A;Molecule type: DNA
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Best Local
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                                                                                              GFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELA 187
                                                                                                                                                                                DHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQ
                       PGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAP
                                                                                                                                                  DHNVPTVDRFNIQD-----QIARKQIETLEANCKEFGIEIAGLDSPNNGIVHVIGPEL
                                                                                                                                                                                                                           PKTIIEKIWDAHTVIGEEGKPSLLYIDLHMVHEVTSPQAFEGLRLAGRPVRRPDLTFATM
                                                                                                                                                                                                                                                     PQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATT
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PSVSAKDIILAVIAKYGVDFGTGHVIEFTGEAIRSLSMEERMTICNMSIEAGAKAGLISP
                                                                         GLTQPGKTIVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQTLWQSKPKTMEVRVTGELA
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34.4%; Score 1396; DB 2;
Similarity 59.2%; Pred. No. 6.8e-90;
79; Conservative 58; Mismatches 124
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Laber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M., Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: B69650
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C;Superfamily: aconitate hydratase
C;Keywords: 4Fe-45; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein;
F;347,407,410/Binding site: 4Fe-48 cluster (Cys) (covalent) #status.predict
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Z99118; GB:AL009126; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision
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Best Local
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KGVTAKDVILAVIGKYGVKFGTGYVIEYTGEVFRNMTMDERMTVCNMSIEAGARAGLIAP
                        PGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAP
                                                                                                                                     GFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELA 187
                                                                                                                                                                                                       DHNIPTVNRFEIKD-----EVAKROVTALERNCEEFGVRLADLHSVDQGIVHVVGPEL
                                                                                                                                                                                                                                                        DHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQ
                                                                                                                                                                                                                                                                                                                                          PQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         h 34.4%; Score 1393.5; DB 2; Similarity 56.5%; Pred. No. 1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EC 4.2.1.33) large chain - Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                    129;
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Ferrari,
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Bertero

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C; Accession: G70853
R; Color, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordor, C; Accession: G70853
R; Color, S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Gentles, S.; Hamin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 339, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gent A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-473 <COL>
A; Residues: 1-473 <COL>
A; Residues: 1-473 <COL>
A; Reperimental source: strain H37Rv
C; Generics:
A; Experimental source: strain H37Rv
C; Generics:
A; Gene: leuC
C; Superfamily: aconitate hydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Jesopropylmalate dehydratase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Jesu-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
C;Accession: T45425
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
                                                                                                                       probable leuC protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                  Length 473;
NPDILAPOERCASTSNRNFEGROGAGGRIHLMSPVMAAAAGIVGKLADVRKLT
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122;
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58.3%; Pred. No. 4e-8!
ive 59; Mismatches
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Best Local Similarity 58.3*
Matches 275; Conservative
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larity 58.1%; Pred. No. 3.7e-89;
Conservative 60; Mismatches 129;
                                                                                                                                                                                                                                                                                                   HIAAYQKSTV 497
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A;Reference number: Z16918
A;Accession: T45425
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-476 <PAR>
A;Cross-references: EMBL:Z99263; PIDN:CAB16447.1
A;Experimental source: cosmid B637
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                                                     233 SIEAGARAGMVAPDETTYEFLRDRPHAP--TGKQWDAAVAYWQQLRTDDDAVFDTEVYLD 290
                                                                                                          291 ATSLSPEVTWGTNEGQGVELAASVEDPELMIDDVARQAAEKALAYMDLREGTEVKDIAVD
                                                                                                                          295 AKDIVPTLTWGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVD 354
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